Quantitation of mRNA by Polymerase Chain Reaction. Nonradioactive PCR Methods; Edited by Th. Kohler, D. Lasner, A.-K. Rost, B. Thamm, B. Pustowoit and H. Remke, Springer; Berlin–Heidelberg, 1995. xx + 165 pp. DM 68.00 (pb). ISBN 3-540-59192-3

Although the sensitivity of PCR has rendered it the method of choice in the detection of small amounts of nucleic acid targets, its utility as a quantitative tool has been slower to gain credit. The ability of PCR to make rare sequences detectable, however, makes it extremely challenging to extrapolate the amounts of initial input template molecules from the measured amounts of product molecules after many cycles of amplification. In the past few years a number of PCR strategies based on different methodological and technical approaches have been adopted for the semiquantitative or quantitative analysis of nucleic acids. Despite the development of a variety of procedures, quantitation of RT-PCR products remain difficult.

This text is an excellent comprehensive compilation of current methods for quantitation of messenger RNA. Each section of the book contains a descriptive part with one or a few illustrative figures followed by the corresponding protocols. The handbook may well serve as a laboratory manual with inspiration for both novice an experienced users. It gives the reader an overview of the most used methods together with technical hints and troubleshooting including information about possible pitfalls associated with some of these methods.

The first part of this handbook presents a short concise introduction to the general aspects of PCR, the design of PCR primers and competitor fragments to be used as internal/external standards in the assays and the use of non-isotopic labels. The contexts of the sections are presented with illustrative figures.

The second part describe both the theoretical and practical aspects of different conventional techniques for mRNA analysis. For that purpose different protocols for e.g. RNA isolation and cDNA synthesis are presented together with methods used for qualitative mRNA analysis (RT-PCR, single-tube RT-PCR) as well as methods using non-radioactive labels for detection of amplified PCR products. However, this second part could have benefitted from a brief introduction to RNase inhibitors to give the reader an opportunity for further improvement of RNA handling, isolation and reverse transcription.

The last part of the handbook concerns the quantitative analysis of mRNAs. Most PCR applications for examining gene expression can be divided into two categories, competitive and non-competitive. The described protocols for mRNA quantitation cover to a large extent the range of methods that so far have been published within this area, although this part of the book suffers from an almost complete lack of protocols for statistical validation of quantitation assays.

This handbook covers the methods used for mRNA quantitation nicely, but some experience with the techniques may be necessary to successfully achieve the goal of setting up quantitative mRNA analysis. It would therefore have been appropriate if the authors had spent a few more words discussing advantages and disadvantages of the different methods presented. Altogether this is a timely and good laboratory handbook, which covers one of the most challenging fields in molecular biology.

Niels Rüdiger

Mass Spectrometry in the Biological Sciences; Edited by A.L. Burlinghame and S.A. Carr, Humana Press; Totowa, NJ, 1995. xii + 570 pp. US$ 145.00 (hb). ISBN 0-89603-340-6

This book consists of 26 individual papers presented at the third symposium on Mass Spectrometry in the Biological Sciences by some of the leading research groups using mass spectrometry. Mass spectrometry has in recent years developed into an important tool for structural characterization of biopolymers due to the high sensitivity, speed of analysis and the quality of the structural information obtained. The book gives a detailed insight into the use of mass spectrometry (MS) for a wide array of problems in protein chemistry, immunology, glycobiology as well as studies of human pathogens, lipids, and nucleic acids.

In the first chapters the principles and future developments of time-of-flight MS and Fourier-transform MS are discussed. The next two chapters demonstrate the use of electrospray MS for elucidation of protein folding and molecular interactions. Then follows a series of very exciting chapters dealing with strategies and various approaches for microcharacterization of proteins and peptides. This includes analysis and identification of proteins separated by gel electrophoresis, partial peptide sequencing by MS/MS or by chemical and enzymatic methods, miniaturization of sample handling techniques as well as approaches to optimize the overall sensitivity. The next four chapters concern characterization of protein modifications such as glycosylation, phosphorylation, and deamidation. Then follow several chapters illustrating other applications of MS, including analysis of lipooligosaccharides, phospholipids, pharmacokinetics and quantification of drugs and metabolites. The last two chapters concern the prospects and use of MS for sequencing and characterization of oligonucleotides. In addition, the book contains eleven excellent appendices with structures and molecular masses of common residues and modifications as well as thorough explanations of common terms used in MS.

The book can be read by biochemists without experience in mass spectrometry as well as by experienced mass spectrometrists who want to keep up to date in the field. The general impression of the book is that it gives the reader a good survey of the current status of mass spectrometry as well as of potential applications and future developments. As such, the book can be a helpful source of knowledge and inspiration for scientists interested in mass spectrometry at the pre-and post-graduate levels.

Ejvind Mørtz

Molecular Biology. Current Innovations and Future Trends. Part 2; Edited by A.M. Griffin and H.G. Griffin, Horizon Scientific Press; Norfolk, 1995. 176 pp. £19.99 (pb). ISBN 1 898486 03 4

The number of technologies from which our knowledge of molecular biology stems is growing increasingly large and it must be difficult for scientists coming into the field, and indeed for practising molecular biologists, to keep abreast of current advances. This series of books, of which this volume is the second, attempts to address this by offering a variety of articles covering a number of new aspects thus hoping to keep scientists informed of recent innovations in both the theory and practice of molecular biology techniques.

This slim volume is divided into ten chapters. The first of these deals with various aspects of automated DNA sequencing, whilst high sensitivity protein sequence analysis is dealt with in the second. Chapter three deals with the introduction of DNA into prokaryotic and eukaryotic cells using electroporation techniques. Chapter four covers non-radioactive labelling and detection methods and the fifth chapter deals with PNA (peptide nucleic acids). Chapter six is concerned with magnetic bead technology and the following chapter deals with antisense technology and ribozymes (not ribosomes as the title is given in the contents and page headings). Phylogenetic tree analysis, nucleic acid analysis by HPLC, and protein analysis by NMR are described in chapters eight, nine and ten, respectively. Whilst some of these are not